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(1) GENERAL INFORMATION:

- (i) APPLICANT: Bakker, Alexander B.H.
Phillips, Joseph H.
Lanier, Lewis L.
- (ii) TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
Related Reagents
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 31-JUL-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/089,168
 - (B) FILING DATE: 12-JUN-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/069,692
 - (B) FILING DATE: 16-DEC-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/069,639
 - (B) FILING DATE: 15-DEC-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/063,717
 - (B) FILING DATE: 29-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/054,430
 - (B) FILING DATE: 01-AUG-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0763X
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650)852-9196
 - (B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 79..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GGA CTT GAA CCC TGC AGC AGG CTC CTG CTC CTG CCT CTC CTG	48
Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu	
-26 -25 -20 -15	
CTG GCT GTA AGT GGT CTC CGT CCT GTC CAG GCC CAG GCC CAG AGC GAT	96
Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp	
-10 -5 1 5	
TGC AGT TGC TCT ACG GTG AGC CCG GGC GTG CTG GCA GGG ATC GTG ATG	144
Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met	
10 15 20	
GGA GAC CTG GTG CTG ACA GTG CTC ATT GCC CTG GCC GTG TAC TTC CTG	192
Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu	
25 30 35	
GGC CGG CTG GTC CCT CGG GGG CGA GGG GCT GCG GAG GCA GCG ACC CGG	240
Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg	
40 45 50	
AAA CAG CGT ATC ACT GAG ACC GAG TCG CCT TAT CAG GAG CTC CAG GGT	288
Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly	
55 60 65 70	
CAG AGG TCG GAT GTC TAC AGC GAC CTC AAC ACA CAG AGG CCG TAT TAC	336
Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr	
75 80 85	
AAA TGA	342
Lys	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
-26 -25 -20 -15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
-10 -5 1 5

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
10 15 20

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
25 30 35

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
40 45 50

Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
55 60 65 70

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
75 80 85

Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGCCTGGA CGCTGCGCCA CATCCCACCG GCCCTTACAC TGTGGTGTCC AGCAGCATCC 60

GGCTTCATGG GGGGACTTGA ACCCTGCAGC AGGCTCCTGC TCCTGCCTCT CCTGCTGGCT 120

GTAAGTGGTC TCCGTCCTGT CCAGGCCAG GCCCAGAGCG ATTGCAGTTG CTCTACGGTG 180

AGCCCGGGCG TGCTGGCAGG GATCGTGATG GGAGACCTGG TGCTGACAGT GCTCATTGCC 240

CTGGCCGTGT ACTTCCTGGG CCGGCTGGTC CCTCGGGGGC GAGGGGCTGC GGAGGCAGCG 300

ACCCGGAAAC AGCGTATCAC TGAGACCGAG TCGCCTTATC AGGAGCTCCA GGGTCAGAGG 360
 TCGGATGTCT ACAGCGACCT CAACACACAG AGGCCGTATT ACAAATGAGC CCGAATCATG 420
 ACAGTCAGCA ACATGATACC TGGATCCAGC CATTCCTGAA GCCCANCCTG CACCTCATTC 480
 CAACTCCTAC CGCGATACAG ACCCACAGAG TGCCATCCCT GAGAGACCAG ACCGCTCCCC 540
 AATACTCTCC TAAAATAAAC ATGAAGCACA AAAAAAAAAA AAAAAAAAAAC TCNGGGGGGG 600
 GGCCCGGTTA NCCAATTTGG NCCTAAAG 628

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser
1				5				10						15	
Asp Leu															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..342

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 79..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGG GCT CTG GAG CCC TCC TGG TGC CTT CTG TTC CTT CCT GTC CTC
 Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu

-26 -25	-20	-15	
CTG ACT GTG GGA GGA TTA AGT CCC GTA CAG GCC CAG AGT GAC ACT TTC			96
Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe			
-10	-5	1	5
CCA AGA TGC GAC TGT TCT TCC GTG AGC CCT GGT GTA CTG GCT GGG ATT			144
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile			
10	15	20	
GTT CTG GGT GAC TTG GTG TTG ACT CTG CTG ATT GCC CTG GCT GTG TAC			192
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr			
25	30	35	
TCT CTG GGC CGC CTG GTC TCC CGA GGT CAA GGG ACA GCG GAA GGG ACC			240
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr			
40	45	50	
CGG AAA CAA CAC ATT GCT GAG ACT GAG TCG CCT TAT CAG GAG CTT CAG			288
Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln			
55	60	65	70
GGT CAG AGA CCA GAA GTA TAC AGT GAC CTC AAC ACA CAG AGG CAA TAT			336
Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr			
75	80	85	
TAC AGA TGA			345
Tyr Arg			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu	
-26 -25	-20 -15
Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe	
-10	-5 1 5
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile	
10	15 20
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr	
25	30 35
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr	
40	45 50
Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln	

55

60

65

70

Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr
 75 80 85

Tyr Arg

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 63..338

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 117..338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACCTGG ACTTCTCTGG ACCACAGTCC TCTGCCAGAC CCCTGCCAGA CCCAGTCCA	60
CC ATG ATC CAT CTG GGT CAC ATC CTC TTC CTG CTT TTG CTC CCA GTG	107
Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val	
-18 -15 -10 -5	
GCT GCA GCT CAG ACG ACT CCA GGA GAG AGA TCA TCA CTC CCT GCC TTT	155
Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe	
1 5 10	
TAC CCT GGC ACT TCA GGC TCT TGT TCC GGA TGT GGG TCC CTC TCT CTG	203
Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu	
15 20 25	
CCG CTC CTG GCA GGC CTC GTG GCT GCT GAT GCG GTG GCA TCG CTG CTC	251
Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu	
30 35 40 45	
ATC GTG GGG GCG GTG TTC CTG TGC GCA CGC CCA CGC CGC AGC CCC GCC	299
Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala	
50 55 60	
CAA GAT GGC AAA GTC TAC ATC AAC ATG CCA GGC AGG GGC TGACCCTCCT	348
Gln Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly	
65 70	
GCAGCTTGA CCTTTGACTT CTGACCCTCT CATCCTGGAT GGTGTGTGGT GCACAGGAAA	408

CCCCGCCCCA ACTTTTGGAT TGTAATAAAA CATTTGAAAC ACA

451

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
-18 -15 -10 -5
Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 1 5 10
Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
15 20 25 30
Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 35 40 45
Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 50 55 60
Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 109..345

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 163..345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCACCATCG GGGTGACATC CGTCCTAGCT GCCTCTCTTC TCCTCTACTG TTCTGAGGAC
TTCCCTGGAC CACAGTTTTG GCCAGATCCC TTCAGGTCCC AGCCCAGC ATG GAC CCC
Met Asp Pro

60

117

CCA GGC TAC CTC CTG TTC CTG CTT CTG CTC CCA GTG GCT GCA AGT CAG	165
Pro Gly Tyr Leu Leu Phe Leu Leu Leu Leu Pro Val Ala Ala Ser Gln	
-15 -10 -5 1	
ACA TCG GCA GGT TCC TGC TCC GGA TGT GGG ACT CTG TCT CTG CCA CTC	213
Thr Ser Ala Gly Ser Cys Ser Gly Cys Gly Thr Leu Ser Leu Pro Leu	
5 10 15	
CTG GCA GGC CTA GTG GCT GCA GAT GCG GTC ATG TCA CTC CTA ATT GTA	261
Leu Ala Gly Leu Val Ala Ala Asp Ala Val Met Ser Leu Leu Ile Val	
20 25 30	
GGG GTG GTG TTT GTA TGT ATG CGC CCA CAC GGC AGG CCT GCC CAA GAA	309
Gly Val Val Phe Val Cys Met Arg Pro His Gly Arg Pro Ala Gln Glu	
35 40 45	
GAT GGT AGA GTC TAC ATC AAC ATG CCT GGC AGA GGC TGACCACGGC	355
Asp Gly Arg Val Tyr Ile Asn Met Pro Gly Arg Gly	
50 55 60	
ACCTTCTGAC CCGCTCATCC TGGATCCTGT GGGTTTGGGG TGCCTGGG	403

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Asp Pro Pro Gly Tyr Leu Leu Phe Leu Leu Leu Leu Pro Val Ala	
-18 -15 -10 -5	
Ala Ser Gln Thr Ser Ala Gly Ser Cys Ser Gly Cys Gly Thr Leu Ser	
1 5 10	
Leu Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Met Ser Leu	
15 20 25 30	
Leu Ile Val Gly Val Val Phe Val Cys Met Arg Pro His Gly Arg Pro	
35 40 45	
Ala Gln Glu Asp Gly Arg Val Tyr Ile Asn Met Pro Gly Arg Gly	
50 55 60	

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 157..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCTTAGCGT GGTCGCGGCC GAGGTGGCAA AAGGAGCATA TTCTCAGGAG ACGGGGCCCC	60
TGCCTGCCAC ACCAAGCATT AGGCCACCAG GAAGACCCCC ATCTGCAAGC AAGCCTAGCC	120
TTCCAGGGAG AAAGAGGCCT CTGCAGCTCC TTCATC ATG AAC TGG CAC ATG ATC	174
Met Asn Trp His Met Ile	
1 5	
ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA ATG ACC TTA	222
Ile Ser Gly Leu Ile Val Val Val Leu Lys Val Val Gly Met Thr Leu	
10 15 20	
TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC	270
Phe Leu Leu Tyr Phe Pro Gln Ile Phe Asn Lys Ser Asn Asp Gly Phe	
25 30 35	
ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT	318
Thr Thr Thr Arg Ser Tyr Gly Thr Val Ser Gln Ile Phe Gly Ser Ser	
40 45 50	
TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC	366
Ser Pro Ser Pro Asn Gly Phe Ile Thr Thr Arg Ser Tyr Gly Thr Val	
55 60 65 70	
TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC	414
Cys Pro Lys Asp Trp Glu Phe Tyr Gln Ala Arg Cys Phe Phe Leu Ser	
75 80 85	
ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA	462
Thr Ser Glu Ser Ser Trp Asn Glu Ser Arg Asp Phe Cys Lys Gly Lys	
90 95 100	
GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG TTT CTT CAG	510
Gly Ser Thr Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Phe Leu Gln	
105 110 115	
GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT	558
Asp Ile Thr Asp Ala Glu Lys Tyr Phe Ile Gly Leu Ile Tyr His Arg	
120 125 130	
GAA GAG AAA AGG TGG CGT TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT	606
Glu Glu Lys Arg Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn	
135 140 145 150	
GTT ACC AAT CAG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA	654
Val Thr Asn Gln Asn Gln Asn Phe Asn Cys Ala Thr Ile Gly Leu Thr	
155 160 165	

AAG ACC TTT GAT GCT GCA TCA TGT GAC ATC AGC TAC CGC AGG ATC TGT 702
 Lys Thr Phe Asp Ala Ala Ser Cys Asp Ile Ser Tyr Arg Arg Ile Cys
 170 175 180

GAG AAG AAT GCC AAA TGATCACAGT TCCCTGTGAC AAGAACTATA CTTGCAACTC 757
 Glu Lys Asn Ala Lys
 185

TTTTTGAATC CATAACAGGT CGTACTGGCC AATGATTACT TTTACTTACC TATCTGTACT 817

ACCAGTAGCG GTCCTTGCCC ATTTGGGAAA CTGAGCTTCT TTCTTCTGCA CTGGGGGACT 877

GGATGCTAGC CATCTCCAGG AGACAGGATC AGTTTTACGG AAACAACTCA GTTAGTATAG 937

AGATGAGGTC CGCTTCTGTA GTACCTTCCT TCAAATAAAG AAATTTGGTA CCTGCCCGG 996

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asn Trp His Met Ile Ile Ser Gly Leu Ile Val Val Val Leu Lys
 1 5 10 15

Val Val Gly Met Thr Leu Phe Leu Leu Tyr Phe Pro Gln Ile Phe Asn
 20 25 30

Lys Ser Asn Asp Gly Phe Thr Thr Thr Arg Ser Tyr Gly Thr Val Ser
 35 40 45

Gln Ile Phe Gly Ser Ser Ser Pro Ser Pro Asn Gly Phe Ile Thr Thr
 50 55 60

Arg Ser Tyr Gly Thr Val Cys Pro Lys Asp Trp Glu Phe Tyr Gln Ala
 65 70 75 80

Arg Cys Phe Phe Leu Ser Thr Ser Glu Ser Ser Trp Asn Glu Ser Arg
 85 90 95

Asp Phe Cys Lys Gly Lys Gly Ser Thr Leu Ala Ile Val Asn Thr Pro
 100 105 110

Glu Lys Leu Phe Leu Gln Asp Ile Thr Asp Ala Glu Lys Tyr Phe Ile
 115 120 125

Gly Leu Ile Tyr His Arg Glu Lys Arg Trp Arg Trp Ile Asn Asn
 130 135 140

Ser Val Phe Asn Gly Asn Val Thr Asn Gln Asn Gln Asn Phe Asn Cys
 145 150 155 160

Ala Thr Ile Gly Leu Thr Lys Thr Phe Asp Ala Ala Ser Cys Asp Ile
165 170 175

Ser Tyr Arg Arg Ile Cys Glu Lys Asn Ala Lys
180 185

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 140..709

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 221
- (D) OTHER INFORMATION: /note= "short form variant lacks nucleotides 221-295"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "short form variant difference at nucleotides 29-35 reads CAGAAGA; 107-109 reads AGA; 128-129 reads AT; 820-826 reads CATAGGT; lacks 859; and 879-880 reads CA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGGACATTAC CGAGCAGGAG CATACATTTC CAGAGCAAGG AGCCCTGCTC GCTGCACCGA	60
ATATCTTATC AAAAAGACTC CTATCTGTAT GCCAACCCAG ACTTCCCAGA AGAGATCAGA	120
TCCCTGATCC CCCATCATC ATG AAC TGG CAC ATG ATC ATC TCG GGG CTT ATC	172
Met Asn Trp His Met Ile Ile Ser Gly Leu Ile	
1 5 10	
GTA GTA GTG ATC AAA GTT GTT GGA ATG ACC TTT TTT CTG CTG TAT TTC	220
Val Val Val Ile Lys Val Val Gly Met Thr Phe Phe Leu Leu Tyr Phe	
15 20 25	
CCA CAG GTT TTT GGC AAA AGT AAT GAT GGC TTC GTC CCC ACG GAG AGC	268
Pro Gln Val Phe Gly Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser	
30 35 40	
TAC GGA ACC ACT AGT GTG CAG AAT GTC TCA CAG ATC TTT GGG AGA AAT	316
Tyr Gly Thr Thr Ser Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn	
45 50 55	

GAC GAA AGT ACC ATG CCT ACA AGG AGC TAT GGA ACA GTC TGT CCC AGA	364
Asp Glu Ser Thr Met Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg	
60 65 70 75	
AAC TGG GAT TTT CAC CAA GGA AAA TGC TTT TTC TTC TCC TTC TCC GAA	412
Asn Trp Asp Phe His Gln Gly Lys Cys Phe Phe Phe Ser Phe Ser Glu	
80 85 90	
TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA	460
Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr	
95 100 105	
CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA	508
Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile	
110 115 120	
GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG	556
Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu	
125 130 135	
AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC	604
Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr	
140 145 150 155	
AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA	652
Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr	
160 165 170	
TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG	700
Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met	
175 180 185	
AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA	749
Asn Ala Lys	
190	
GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAA TATAGAGCAT CAAAGACTGT	809
GCCCATCTTC ATAGGTGGGA GTTCCCTATT GAATCCTCAA AGTCAATTTT GTTACTCCAC	869
AAACATCTTA CCATAGTAAA ACTCCCT	896

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Asn	Trp	His	Met	Ile	Ile	Ser	Gly	Leu	Ile	Val	Val	Val	Ile	Lys
1				5				10						15	

Val	Val	Gly	Met	Thr	Phe	Phe	Leu	Leu	Tyr	Phe	Pro	Gln	Val	Phe	Gly			
			20					25					30					
Lys	Ser	Asn	Asp	Gly	Phe	Val	Pro	Thr	Glu	Ser	Tyr	Gly	Thr	Thr	Ser			
		35					40					45						
Val	Gln	Asn	Val	Ser	Gln	Ile	Phe	Gly	Arg	Asn	Asp	Glu	Ser	Thr	Met			
	50					55					60							
Pro	Thr	Arg	Ser	Tyr	Gly	Thr	Val	Cys	Pro	Arg	Asn	Trp	Asp	Phe	His			
	65				70					75					80			
Gln	Gly	Lys	Cys	Phe	Phe	Phe	Ser	Phe	Ser	Glu	Ser	Pro	Trp	Lys	Asp			
				85					90					95				
Ser	Met	Asp	Tyr	Cys	Ala	Thr	Gln	Gly	Ser	Thr	Leu	Ala	Ile	Val	Asn			
		100						105					110					
Thr	Pro	Glu	Lys	Leu	Lys	Tyr	Leu	Gln	Asp	Ile	Ala	Gly	Ile	Glu	Asn			
		115					120					125						
Tyr	Phe	Ile	Gly	Leu	Val	Arg	Gln	Pro	Gly	Glu	Lys	Lys	Trp	Arg	Trp			
	130					135					140							
Ile	Asn	Asn	Ser	Val	Phe	Asn	Gly	Asn	Val	Thr	Asn	Gln	Asp	Gln	Asn			
	145				150					155				160				
Phe	Asp	Cys	Val	Thr	Ile	Gly	Leu	Thr	Lys	Thr	Tyr	Asp	Ala	Ala	Ser			
				165					170					175				
Cys	Glu	Val	Ser	Tyr	Arg	Trp	Ile	Cys	Glu	Met	Asn	Ala	Lys					
			180					185					190					